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## SEQUENCE LISTING

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<120> GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY

<130> 001560-377

<140> US 09/446,089

<141> 1999-12-17

<150> PCT/JP99/02045

<151> 1999-04-16

<150> JP 10/107296

<151> 1998-04-17

<160> 15

<170> PatentIn version 3.0

<210> 1

<211> 1951

<212> DNA

<213> Antirrhinum majus

<220>

<221> CDS

<222> (96)..(1781)

<400> 1

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Met Phe Lys Asn Pro Asn  
1 5

atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa 161  
Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu  
10 15 20

tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc 209  
Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe  
25 30 35

cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg 257  
Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg  
40 45 50

ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa 305  
Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys

55	60	65	70	
tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt				353
Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys	75	80	85	
ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc				401
Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser	90	95	100	
act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac				449
Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr	105	110	115	
att gcc aaa ttc aag aaa gcc gtt gag ctt atg cga gct cta cct gag				497
Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu	120	125	130	
gat gac cct cgt agc ttc aag caa caa gct aac gtc cat tgc gct tac				545
Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr	135	140	145	150
tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa				593
Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln	155	160	165	
atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac				641
Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr	170	175	180	
ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct				689
Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala	185	190	195	
ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca				737
Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser	200	205	210	
atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt				785
Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser	215	220	225	230
aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat				833
Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp	235	240	245	
tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa				881
Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys	250	255	260	
att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc				929
Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe	265	270	275	
ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg				977
Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly	280	285	290	

tcg att gag tta gtc cct cat ggc atg ata cat tta tgg acc ggt tct Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser 295 300 305 310	1025
gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct Glu Asn Thr Pro Tyr Phe Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala 315 320 325	1073
aga gac ccg ata ttt ttt gct cat cat tgc aac gtc gat aga atg tgg Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp 330 335 340	1121
tcc ata tgg aag acc cta gga ggg ccg cgg agg acg gac tta aca gat Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp 345 350 355	1169
cca gat ttt ctt gat gcg tct ttc gtt ttt tat gac gaa aac gca gag Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu 360 365 370	1217
atg gtt cgg gtc aag gtt cgg gat tgc tta gat gaa aag aaa cta ggg Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly 375 380 385 390	1265
tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr 395 400 405	1313
cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr 410 415 420	1361
gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys 425 430 435	1409
gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp 440 445 450	1457
gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp 455 460 465 470	1505
cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp 475 480 485	1553
ctt gcg gtg att tgc ccg gag aat gct gag ttc gcc ggg agt ttc gtg Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val 490 495 500	1601
agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu 505 510 515	1649
tta aca ttg tgc att tgt gat att ttg gag gat ttg gat gct gac gaa	1697

Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu  
 520 525 530  
 gat gat tat gtg ttg gtc act ttg gtt ccg aga aac gcc gga gat gcg 1745  
 Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala  
 535 540 545 550  
 atc aag att cat aat gtc aag att gag ctt gat ggc taataaattc 1791  
 Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly  
 555 560  
 tattgatttc ttctcaacct acagttgatc atttaccgat tgattattcc aataaaagta 1851  
 tctcatgtac caatatcgat cgtattaatc gtaatacttt cagattttta tttattttaa 1911  
 agcagttgta taaatgggtga aataaggatt actttttgag 1951  
  
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 <211> 562  
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 <213> Antirrhinum majus  
  
 <400> 2  
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 1 5 10 15  
 Asn Asp Asn Asp Gln Glu Ser Ser His Arg Cys Lys His Ile Leu Leu  
 20 25 30  
 Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn  
 35 40 45  
 Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala  
 50 55 60  
 Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr  
 65 70 75 80  
 Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe  
 85 90 95  
 Glu Leu Pro Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His  
 100 105 110  
 Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu  
 115 120 125

Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala  
 130 135 140

Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe  
 145 150 155 160

Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe  
 165 170 175

His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile  
 180 185 190

Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly  
 195 200 205

Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr  
 210 215 220

Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu  
 225 230 235 240

Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln  
 245 250 255

Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala  
 260 265 270

Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln  
 275 280 285

Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile  
 290 295 300

His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly  
 305 310 315 320

Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser  
 325 330 335

Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg  
 340 345 350

Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe

355                      360                      365  
 Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu  
     370                              375                      380  
 Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp  
     385                              390                      395                      400  
 Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys  
                             405                              410                      415  
 Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile  
                             420                              425                              430  
 Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg  
                             435                              440                              445  
 Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly  
                             450                              455                              460  
 Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile  
     465                              470                              475                              480  
 Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu  
                             485                              490                              495  
 Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys  
                             500                              505                              510  
 Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu  
                             515                              520                              525  
 Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro  
                             530                              535                              540  
 Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu  
     545                              550                              555                              560

Asp Gly

<210> 3  
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 <212> PRT

<213> Antirrhinum majus

<400> 3

Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro  
1 5 10

<210> 4

<211> 12

<212> PRT

<213> Antirrhinum majus

<400> 4

Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys  
1 5 10

<210> 5

<211> 18

<212> PRT

<213> Antirrhinum majus

<400> 5

Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln  
1 5 10 15

Glu Phe

<210> 6

<211> 29

<212> PRT

<213> Antirrhinum majus

<220>

<221> UNSURE

<222> (8)..(8)

<223> Amino acid 8 is Xaa wherein Xaa = unknown or other.

<220>

<221> UNSURE

<222> (28)..(28)

<223> Amino acid 28 is Xaa wherein Xaa = unknown or other.

<400> 6

Lys Ile Asp Phe Glu Leu Pro Xaa Pro Ser Thr Thr Met Arg Val Arg  
1 5 10 15

Arg Ala Ala His Leu Val Asp Asp Ala Tyr Ile Xaa Lys  
20 25

<210> 7

<211> 125  
 <212> PRT  
 <213> Antirrhinum majus

<400> 7

Arg	Gln	Met	Val	Ser	Ser	Ala	Lys	Thr	Pro	Gln	Leu	Phe	Phe	Gly	Arg
1				5					10					15	
Pro	Tyr	Arg	Arg	Gly	Asp	Gln	Glu	Phe	Pro	Gly	Val	Gly	Ser	Ile	Glu
			20					25					30		
Leu	Val	Pro	His	Gly	Met	Ile	His	Leu	Trp	Thr	Gly	Ser	Glu	Asn	Thr
		35					40					45			
Pro	Tyr	Gly	Glu	Asn	Met	Gly	Ala	Phe	Tyr	Ser	Thr	Ala	Arg	Asp	Pro
	50					55					60				
Ile	Phe	Phe	Ala	His	His	Ser	Asn	Val	Asp	Arg	Met	Trp	Ser	Ile	Trp
65					70				75					80	
Lys	Thr	Leu	Gly	Gly	Pro	Arg	Arg	Thr	Asp	Leu	Thr	Asp	Pro	Asp	Phe
			85						90					95	
Leu	Asp	Ala	Ser	Phe	Val	Phe	Cys	Asp	Glu	Asn	Ala	Glu	Met	Val	Arg
		100						105					110		
Val	Lys	Val	Arg	Asp	Cys	Leu	Asp	Gly	Lys	Lys	Leu	Gly			
	115						120					125			

<210> 8  
 <211> 7  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Primer

<220>  
 <221> PEPTIDE  
 <222> (2)..(2)  
 <223> Amino acid 2 is Xaa wherein Xaa = Val or Ile.

<400> 8

Phe	Xaa	Lys	Phe	Thr	Ala	Ile
1				5		

<210> 9  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Primer



<220>  
 <221> PEPTIDE  
 <222> (6)..(6)  
 <223> Amino acid 6 is Xaa wherein Xaa = Thr or Pro.

<400> 9

Lys Trp Lys Gly Lys Xaa  
 1 5

<210> 10  
 <211> 6  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Primer

<400> 10

His Ala Val Cys Asn Glu  
 1 5

<210> 11  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<220>  
 <221> misc\_feature  
 <222> (6)..(18)  
 <223> Nucleotides 6, 15 and 18 are "n" wherein "n" = a or c or g  
 or t/u or unknown or other

<400> 11  
 ttyrtnaart tyacngcnat

20

<210> 12  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer

<220>  
 <221> misc\_feature  
 <222> (12)..(12)  
 <223> Nucleotide 12 is "n" wherein "n" = a or c or g or t/u

or unknown or other

<400> 12  
aartggaarg gnaarmc 17

<210> 13  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<220>  
<221> misc\_feature  
<222> (4)..(7)  
<223> Nucleotides 4 and 7 are "n" wherein "n" = a or c or g or  
t/u or unknown or other

<400> 13  
rtgngcnacr carttctc 18

<210> 14  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 14  
aaggatccgg ccctatcgcc 20

<210> 15  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Primer

<400> 15  
gggttcgaag aattcatctc tg 22